RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,263 TIME: 13:27:57

Input Set : A:\PF140 NewSeq050801.txt **ENTERED**
Output Set: N:\CRF3\07232001\I895263.raw

SEQUENCE LISTING

```
 4 (1) GENERAL INFORMATION:
 6      (i) APPLICANT: He, Wei-Wu et al.
 8     (ii) TITLE OF INVENTION: Interleukin-1 Beta Converting Enzyme
 9                              Like Apoptosis Protease 3 and 4
11    (iii) NUMBER OF SEQUENCES: 12
13     (iv) CORRESPONDENCE ADDRESS:
14          (A) ADDRESSEE: Human Genome Sciences, Inc.
15          (B) STREET: 9410 Key West Ave.
16          (C) CITY: Rockville
17          (D) STATE: MD
18          (E) COUNTRY: USA
19          (F) ZIP: 20850
21      (v) COMPUTER READABLE FORM:
22          (A) MEDIUM TYPE: Floppy disk
23          (B) COMPUTER: IBM PC compatible
24          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27     (vi) CURRENT APPLICATION DATA:
C--> 28     (A) APPLICATION NUMBER: US/09/895,263
C--> 29     (B) FILING DATE: 02-Jul-2001
30          (C) CLASSIFICATION:
32    (vii) PRIOR APPLICATION DATA:
33          (A) APPLICATION NUMBER:
34          (B) FILING DATE:
36   (viii) ATTORNEY/AGENT INFORMATION:
37          (A) NAME: Jonathan L. Klein
38          (B) REGISTRATION NUMBER: 41,119
39          (C) REFERENCE/DOCKET NUMBER: PF140
41     (ix) TELECOMMUNICATION INFORMATION:
42          (A) TELEPHONE: 301-251-6015
43          (B) TELEFAX: 301-309-8439
46 (2) INFORMATION FOR SEQ ID NO: 1:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 1369 base pairs
50          (B) TYPE: nucleic acid
51          (C) STRANDEDNESS: single
52          (D) TOPOLOGY: linear
54     (ii) MOLECULE TYPE: DNA (genomic)
57     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
59 GCACGAGAAA CTTTGCTGTG CGCGTTCTCC CGCGCGCGGG CTCAACTTTG TAGAGCGAGG 60
61 GGCCAACTTG GCAGAGCGCG CGGCCAGCTT TGCAGAGAGC GCCCTCCAGG GACTATGCGT 120
63 GCGGGGACAC GGGTCGCTTT GGGCTCTTCC ACCCCTGCGG AGCGCACTAC CCCGAGCCAG 180
65 GGGCGGTGCA AGCCCCGCCC GGCCCTACCC AGGGCGGCTC CTCCCTCCGC AGCGCCGAGA 240
67 CTTTTAGTTT CGCTTTCGCT AAAGGGGCCC CAGACCCTTG CTGCGGAGCG ACGGAGAGAG 300
69 ACTGTGCCAG TCCCAGCCGC CCTACCGCCG TGGGAACGAT GGCAGATGAT CAGGGCTGTA 360
71 TTGAAGAGCA GGGGGTTGAG GATTCAGCAA ATGAAGATTC AGTGGATGCT AAGCCAGACC 420
```

RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,263   TIME: 13:27:57

Input Set : A:\PF140 NewSeq050801.txt
Output Set: N:\CRF3\07232001\I895263.raw

```
 73 GGTCCTCGTT TGTACCGTCC CTCTTCAGTA AGAAGAAGAA AAATGTCACC ATGCGATCCA  480
 75 TCAAGACCAC CCGGGACCGA GTGCCTACAT ATCAGTACAA CATGAATTTT GAAAAGCTGG  540
 77 GCAAATGCAT CATAATAAAC AACAAGAACT TTGATAAAGT GACAGGTATG GGCGTTCGAA  600
 79 ACGGAACAGA CAAAGATGCC GAGGCGCTCT TCAAGTGCTT CCGAAGCCTG GGTTTTGACG  660
 81 TGATTGTCTA TAATGACTGC TCTTGTGCCA AGATGCAAGA TCTGCTTAAA AAAGCTTCTG  720
 83 AAGAGGACCA TACAAATGCC GCCTGCTTCG CCTGCATCCT CTTAAGCCAT GGAGAAGAAA  780
 85 ATGTAATTTA TGGGAAAGAT GGTGTCACAC CAATAAAGGA TTTGACAGCC CACTTTAGGG  840
 87 GGGATAGATG CAAAACCCTT TTAGAGAAAC CCAAACTCTT CTTCATTCAG GCTTGCCGAG  900
 89 GGACCGAGCT TGATGATGCC ATCCAGGCCG ACTCGGGGCC CATCAATGAC ACAGATGCTA  960
 91 ATCCTCGATA CAAGATCCCA GTGGAAGCTG ACTTCCTCTT CGCCTATTCC ACGGTTCCAG 1020
 93 GCTATTACTC GTGGAGGAGC CCAGGAAGAG GCTCCTGGTT TGTGCAAGCC CTCTGCTCCA 1080
 95 TCCTGGAGGA GCACGGAAAA GAGCTGGAAA TCATGCAAAT CCTCACCAGG GTGAATGACA 1140
 97 GAGTTGCCAG GCACTTTGAG TCTCAGTCTG ATGACCCACA CTTCCATGAG AAGAAGCAGA 1200
 99 TCCCCTGTGT GGTCTCCATG CTCACCAAGG AACTCTACTT CAGTCAATAG CCATATCAGG 1260
101 GGTACATTCT AGCTGAGAAG CAATGGGTCA CTCATTAATG AATCACATTT TTTTATGCTC 1320
103 TTGAAATATT CAGAAATTCT CCAGGATTTT AATTTCAGGA AAATGTATT           1369
106 (2) INFORMATION FOR SEQ·ID NO: 2:
108        (i) SEQUENCE CHARACTERISTICS:
109             (A) LENGTH: 303 amino acids
110             (B) TYPE: amino acid
111             (C) STRANDEDNESS: single
112             (D) TOPOLOGY: linear
114        (ii) MOLECULE TYPE: protein
117        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
119        Met Ala Asp Asp Gln Gly Cys Ile Glu Glu Gln Gly Val Glu Asp Ser
120        1                   5                   10                  15
122        Ala Asn Glu Asp Ser Val Asp Ala Lys Pro Asp Arg Ser Ser Phe Val
123                     20                  25                  30
125        Pro Ser Leu Phe Ser Lys Lys Lys Lys Asn Val Thr Met Arg Ser Ile
126                 35                  40                  45
128        Lys Thr Thr Arg Asp Arg Val Pro Thr Tyr Gln Tyr Asn Met Asn Phe
129              50                  55                  60
131        Glu Lys Leu Gly Lys Cys Ile Ile Ile Asn Asn Lys Asn Phe Asp Lys
132        65                  70                  75                  80
134        Val Thr Gly Met Gly Val Arg Asn Gly Thr Asp Lys Asp Ala Glu Ala
135                     85                  90                  95
137        Leu Phe Lys Cys Phe Arg Ser Leu Gly Phe Asp Val Ile Val Tyr Asn
138                     100                 105                 110
140        Asp Cys Ser Cys Ala Lys Met Gln Asp Leu Leu Lys Lys Ala Ser Glu
141                 115                 120                 125
143        Glu Asp His Thr Asn Ala Ala Cys Phe Ala Cys Ile Leu Leu Ser His
144              130                 135                 140
146        Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys
147        145                 150                 155                 160
149        Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu
150                     165                 170                 175
152        Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp
153                 180                 185                 190
155        Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn
```

```
156              195              200              205
158      Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser
159          210              215              220
161      Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp
162      225              230              235              240
164      Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Glu Leu
165              245              250              255
167      Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His
168              260              265              270
170    · Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile
171          275              280              285
173      Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln
174          290              295              300
176 (2) INFORMATION FOR SEQ ID NO: 3:
178      (i) SEQUENCE CHARACTERISTICS:
179          (A) LENGTH: 1159 base pairs
180          (B) TYPE: nucleic acid
181          (C) STRANDEDNESS: single
182          (D) TOPOLOGY: linear
184      (ii) MOLECULE TYPE: DNA (genomic)
187      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
189 GCACGAGCGG ATGGGTGCTA TTGTGAGGCG GTTGTAGAAG AGTTTCGTGA GTGCTCGCAG      60
191 CTCATACCTG TGGCTGTGTA TCCGTGGCCA CAGCTGGTTG GCGTCGCCTT GAAATCCCAG     120
193 GCCGTGAGGA GTTAGCGAGC CCTGCTCACA CTCGGCGCTC TGGTTTTCGG TGGGTGTGCC     180
195 CTGCACCTGC CTCTTCCCGC ATTCTCATTA ATAAAGGTAT CCATGGAGAA CACTGAAAAC     240
197 TCAGTGGATT CAAAATCCAT TAAAAATTTG GAACCAAAGA TCATACATGG AAGCGAATCA     300
199 ATGGACTCTG GAATATCCCT GGACAACAGT TATAAAATGG ATTATCCTGA GATGGGTTTA     360
201 TGTATAATAA TTAATAATAA GAATTTTCAT AAAAGCACTG GAATGACATC TCGGTCTGGT     420
203 ACAGATGTCG ATGCAGCAAA CCTCAGGGAA ACATTCAGAA ACTTGAAATA TGAAGTCAGG     480
205 AATAAAAATG ATCTTACACG TGAAGAAATT GTGGAATTGA TGCGTGATGT TTCTAAAGAA     540
207 GATCACAGCA AAAGGAGCAG TTTTGTTTGT GTGCTTCTGA GCCATGGTGA AGAAGGAATA     600
209 ATTTTTGGAA CAAATGGACC TGTTGACCTG AAAAAAATAA CAAACTTTTT CAGAGGGGAT     660
211 CGTTGTAGAA GTCTAACTGG AAAACCCAAA CTTTTCATTA TTCAGGCCTG CCGTGGTACA     720
213 GAACTGGACT GTGGCATTGA GACAGACAGT GGTGTTGATG ATGACATGGC GTGTCATAAA     780
215 ATACCAGTGG AGGCCGACTT CTTGTATGCA TACTCCACAG CACCTGGTTA TTATTCTTGG     840
217 CGAAATTCAA AGGATGGCTC CTGGTTCATC CAGTCGCTTT GTGCCATGCT GAAACAGTAT     900
219 GCCGACAAGC TTGAATTTAT GCACATTCTT ACCCGGGTTA ACCGAAAGGT GGCAACAGAA     960
221 TTTGAGTCCT TTTCCTTTGA CGCTACTTTT CATGCAAAGA AACAGATTCC ATGTATTGTT    1020
223 TCCATGCTCA CAAAAGAACT CTATTTTTAT CACTAAAGAA ATGGTTGGTT GGTGGTTTTT    1080
225 TTTAGTTTGT ATGCCAAGTG AGAAGATGGT ATATTTGGGT ACTGTATTTC CCTCTCATTG    1140
227 GGGACCTACT CTCATGCTG                                                 1159
229 (2) INFORMATION FOR SEQ ID NO: 4:
231      (i) SEQUENCE CHARACTERISTICS:
232          (A) LENGTH: 277 amino acids
233          (B) TYPE: amino acid
234          (C) STRANDEDNESS: single
235          (D) TOPOLOGY: linear
237      (ii) MOLECULE TYPE: protein
240      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
```

RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,263   TIME: 13:27:57

Input Set : **A:\PF140 NewSeq050801.txt**
Output Set: **N:\CRF3\07232001\I895263.raw**

```
242        Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu
243        1                   5                   10                  15
245        Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser
246                    20                  25                  30
248        Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile
249                    35                  40                  45
251        Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg
252            50                  55                  60
254        Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn
255        65                  70                  75                  80
257        Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile
258                    85                  90                  95
260        Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser
261                    100                 105                 110
263        Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
264                    115                 120                 125
266        Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
267            130                 135                 140
269        Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
270        145                 150                 155                 160
272        Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
273                    165                 170                 175
275        Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp
276                    180                 185                 190
278        Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
279                    195                 200                 205
281        Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
282            210                 215                 220
284        Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
285        225                 230                 235                 240
287        Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
288                    245                 250                 255
290        His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu
291                    260                 265                 270
293        Leu Tyr Phe Tyr His
294                    275
296 (2) INFORMATION FOR SEQ ID NO: 5:
298        (i) SEQUENCE CHARACTERISTICS:
299            (A) LENGTH: 31 base pairs
300            (B) TYPE: nucleic acid
301            (C) STRANDEDNESS: single
302            (D) TOPOLOGY: linear
304        (ii) MOLECULE TYPE: DNA (genomic)
307        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
309 GATCGGATCC ATGCGTGCGG GGACACGGGT C                                  31
311 (2) INFORMATION FOR SEQ ID NO: 6:
313        (i) SEQUENCE CHARACTERISTICS:
314            (A) LENGTH: 31 base pairs
315            (B) TYPE: nucleic acid
```

RAW SEQUENCE LISTING   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,263   TIME: 13:27:57

Input Set : A:\PF140 NewSeq050801.txt
Output Set: N:\CRF3\07232001\I895263.raw

```
316            (C) STRANDEDNESS: single
317            (D) TOPOLOGY: linear
319      (ii) MOLECULE TYPE: DNA (genomic)
322      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
324 GTACTCTAGA TCATTCACCC TGGTGGAGGA T                              31
326 (2) INFORMATION FOR SEQ ID NO: 7:
328        (i) SEQUENCE CHARACTERISTICS:
329            (A) LENGTH: 31 base pairs
330            (B) TYPE: nucleic acid
331            (C) STRANDEDNESS: single
332            (D) TOPOLOGY: linear
334      (ii) MOLECULE TYPE: DNA (genomic)
337      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
339 GATCGGATCC ATGGAGAACA CTGAAAACTC A                              31
341 (2) INFORMATION FOR SEQ ID NO: 8:
343        (i) SEQUENCE CHARACTERISTICS:
344            (A) LENGTH: 31 base pairs
345            (B) TYPE: nucleic acid
346            (C) STRANDEDNESS: single
347            (D) TOPOLOGY: linear
349      (ii) MOLECULE TYPE: DNA (genomic)
352      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
354 GTACTCTAGA TTAGTGATAA AAATAGAGTT C                              31
356 (2) INFORMATION FOR SEQ ID NO: 9:
358        (i) SEQUENCE CHARACTERISTICS:
359            (A) LENGTH: 22 base pairs
360            (B) TYPE: nucleic acid
361            (C) STRANDEDNESS: single
362            (D) TOPOLOGY: linear
364      (ii) MOLECULE TYPE: DNA (genomic)
367      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
369 GACTATGCGT GCGGGGACAC GG                                        22
371 (2) INFORMATION FOR SEQ ID NO: 10:
373        (i) SEQUENCE CHARACTERISTICS:
374            (A) LENGTH: 53 base pairs
375            (B) TYPE: nucleic acid
376            (C) STRANDEDNESS: single
377            (D) TOPOLOGY: linear
379      (ii) MOLECULE TYPE: DNA (genomic)
382      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
384 AATCAAGCGT AGTCTGGGAC GTCGTATGGG TATTCACCCT GGTGGAGGAT TTG       53
386 (2) INFORMATION FOR SEQ ID NO: 11:
388        (i) SEQUENCE CHARACTERISTICS:
389            (A) LENGTH: 21 base pairs
390            (B) TYPE: nucleic acid
391            (C) STRANDEDNESS: single
392            (D) TOPOLOGY: linear
394      (ii) MOLECULE TYPE: DNA (genomic)
397      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
```

VERIFICATION SUMMARY   DATE: 07/23/2001
PATENT APPLICATION: US/09/895,263   TIME: 13:27:58

Input Set : **A:\PF140 NewSeq050801.txt**
Output Set: **N:\CRF3\07232001\I895263.raw**

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:418 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12 ⎯